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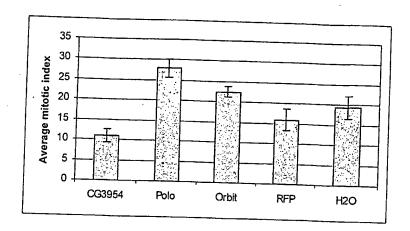
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FIGURE 1

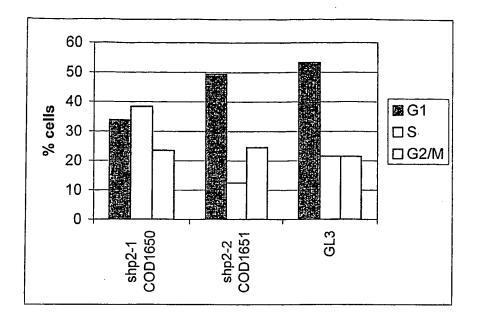


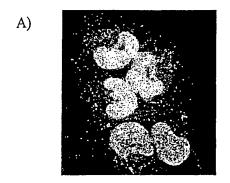
Score = 553 bits (1425), Expect = e-156 Identities = 327/700 (46%), Positives = 406/700 (57%), Gaps = 152/700 (21%)

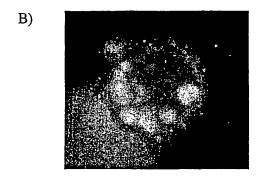
| CONTRACTOR CONTRACTOR | | |
|--|-------------------|--|
| | _ | |
| | | |
| Query: | 1 | MSSRRWFHPTISGIEAEKLLQEQGFDGSFLARLSSSNPGAFTLSVRRGNEVTHIKIQNNG 60 |
| Sbict: | 1 | M+SRRWFHP I+G+EAE LL +G DGSFLAR S SNPG FTLSVRR VTHIKIQN G |
| Beta-strand region | 50 | MTSRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTG 60 |
| Mydrogen bonded turn | 48 | ** |
| Beta-strand region | 41 | ****** |
| lydrogen bonded turn | 38 | •• |
| Beta-strand region | 28 | ***** |
| lydrogen bonded turn | 26 | ** |
| Melical region | 13 | ****** |
| Beta-strand region | 7 | • |
| SH2 1. | 6 | ********* |
| lydrogen bonded turn | 5 | •• |
| TPN11 | 1 | ************************************** |
| Ni o wich | ٠, | NOTE: NO PROPERTY OF THE PROPE |
| wery: | 61 | |
| bjct: | 61 | D++DLYGGEKFATL ELVQYYME+ G+LKEKNG IELK PL CA+PT+ERWFHG+LSGK |
| ydrogen bonded turn | 83 | DYYDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSERWFHGHLSGK 120 |
| elical region | 74 | ******* |
| eta-strand region . | 70 | •• |
| ydrogen bonded turn | 66 | •• |
| eta-strand region | 63 | *** |
| H2 1. | 61 | ********* |
| TPN11 | 61 | +++++++++++++++++++++++++++++++++++++++ |
| ydrogen bonded turn | 85 | ** |
| elical region | 119 | |
| eta-strand region | 113 | |
| H2 2. | 112 | |
| ydrogen bonded turn | 111 | |
| ydrogen bonded turn eta-strand region | 108 | |
| eta-strand region | 95 | ** |
| eta-strand region | 89 | |
| | 0,5 | • |
| iery: | 120 | EAEKLILERGKNGSFLVRESQSKPGDFVLSVRTDDKVTHVMIRWQDKKYD 169 |
| • | | EAEKL+ E+GK+GSFLVRESQS PGDFVLSVRT D KVTHVMIR Q+ KYD |
| ojet: | 121 | EAEKLLTEKGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYD 180 |
| eta-strand region | 147 | ****** |
| ydrogen bonded turn | 144 | •• |
| ata-strand region | 134 | ***** |
| drogen bonded turn | 132 | ** |
| drogen bonded turn | 129 | • |
| elical region | 121 | ******* |
| i2 2. IPN11 | 121 | |
| eta-strand region | 178 | ********** |
| drogen bonded turn | 176 | *** |
| eta-strand region | 166 | *************************************** |
| | | |
| ery: | 170 | VGGGESFGTLSELIDHYKRNPMVETCGTVVHLRQPFNATRITAAGINARVEQLVKGGFWE 229 |
| | | VGGGE F +L++L++HYK+NPMVET GTV+ L+QP N TRI A A +E V+ |
| ojet: | 181 | VGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQPLNTTRINAAEIESRVR 231 |
| lical region | 223 | • ••• |
| ta-strand region | 221 | •• |
| eta-strand region | 214 | •• |
| ta-strand region | 209 | • |
| drogen bonded turn | 205 | ** |
| ta-strand region | 203 | • |
| elical region | 190 | ********* |
| eta-strand region | 187 | |
| PN11 12 2. | 181 | ++++++++++++++++++++++++++++++++++++++ |
| and the second s | 226 | ***** |
| elical region | 220 | |
| ery: | 230 | EFESLQQDSRDTFSRNEGYKQENRLKNRYRNILPYDHTRVKLLDVEHSVAGAEYINANYI 289 |
| | | L + + T +G+ +E + L Y |
| ojet: | 232 | ELSKLAETTDKVKQGFWEEFETLQQQECKLLYSRKE 267 |
| lical region | 266 | *** |
| lical region | 256 | |
| lical region | 247 | ****** |
| PN11 | 232 | |
| | 232 | *** |
| lical region | | |
| - | | RLPTDGDLYNMSSSSESLNSSVPSCPACTAAQTQRNCSNCQLQNKTCVQCAVKSAILPYS 349 |
| elical region mery: | 290 | The transfer of the transfer o |
| ery: | | Q Q N + + +N ILP+ |
| mery: | 268 | Q Q N + + +N ILP+GQRQENKNKNRYKNILPFD 286 |
| ery: ojct: drogen bonded turn | 268 280 | Q Q N + + +N ILP+GQRQENKNKNRYKNILPFD 286 |
| ery: ojct: odrogen bonded turn OTEIN-TYROSINE PHOSPHATASE. | 268 280 276 | Q Q N + + +N ILP+ |
| ery: ojct: drogen bonded turn | 268 280 | Q Q N + + +N ILP+GQRQENKNKNRYKNILPFD 286 |

| Hydrogen bonded turn | 286 | · |
|-------------------------------|-------|--|
| Query: | 350 | NCATCSRKSDSLSKHKRSESSASSSPSSGSGSGPGSSGTSGVSSVNGPGTPTNLTSGTAG 409 |
| | | + D P P + HTRVVLHDGD302 |
| Sbjct: | | HTKVVLHUGD |
| Beta-strand region | 289 | |
| Hydrogen bonded turn | 287 | |
| PTPN11 | | ********* |
| PROTEIN-TYROSINE PHOSPHATASE. | 287 | *************************************** |
| Query: | 410 | CLVGLLKRHSNDSSGAVSISMAERERE-REREMFKTYIATQGCLLTQQVNTVTDFWNNVW 468 |
| | | |
| Sbjct: | | DYINA-NIIMPEFETKCHNSKPKKSYIATQGCLQNTVNDFWRMVF 346 |
| Beta-strand region | 304 | |
| PTPN11 | 303 | |
| PROTEIN-TYROSINE PHOSPHATASE. | | |
| Hydrogen bonded turn | 335 | **** |
| Beta-strand region | 327 | ****** |
| Helical region | 338 | |
| Query: | | QENTRVIVMTTKEYERGKEKCARYWPDEGRSEQFGHARIQCVSENSTSDYTLREFLVSWR 528 QENTRVIVMTTKE ERGK KC +YWPDE +++G R++ V E++ DYTLRE +S |
| Sbjct: | 347 | QENSRVIVMTTKEVERGKSKCVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKV 406 |
| Hydrogen bonded turn | 406 | • |
| Beta-strand region | 396 | |
| Beta-strand region | 383 | ******* |
| Hydrogen bonded turn | 381 | ** |
| Beta-strand region | 377 | *** |
| Hydrogen bonded turn | 374 | ** |
| Beta-strand region | 364 | ** |
| Hydrogen bonded turn | 362 | ** |
| Beta-strand region | 360 | •• |
| Beta-strand region | 352 | **** |
| Hydrogen bonded turn | 349 | • |
| Helical region | 347 | ** |
| PTPN11 | 347 | **** |
| PROTEIN-TYROSINE PHOSPHATASE. | 347 | *************************************** |
| Query: | 529 | DQPARRIFHYHFQVWPDHGVPADPGCVLNFLQDVNTRQSHLAQAGEKPGPICVHCSAG 586 O R ++ YHF+ WPDHGVP+DPG VL+FL++V+ +Q + AG P+ VHCSAG |
| | 407 | GOGNTERTVWQYHFRTWPDHGVPSDPGGVLDFLEEVHHKQESIMDAGPVVVHCSAG 462 |
| Sbjct: | | GGGIEKIANGTUTKINE PROATORIOGE CONTRACTORIOGE CONTRACTORIO CONTRACTORIO CONTRACTORIO CONTRACTORIO |
| Beta-strand region | 407 | |
| Hydrogen bonded turn PTPN11 | 407 | +++++++ |
| PROTETULTVBOSTNE PHOSPHATASE. | 407 | ******** |
| Hydrogen bonded turn | 450 | ** |
| Helical region | 432 | |
| active | 459 | |
| Beta-strand region | 455 | |
| | | IGRTGTFIVIDMILDQIVRNGLDTEIDIQRTIQMVRSQRSGLVQTEAQYKFVYYAVQHYI 646 |
| Query: | | TGRTGTFIVID+++D I G+D +ID+ +TIQMVRSQRSG+VQTEAQY+F+Y AVQHYI |
| Sbjct: | 463 | IGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRFIYMAVQHYI 522 |
| Helical region | 508 | ******* |
| Hydrogen bonded turn | 502 | ** |
| Hydrogen bonded turn | 499 | •• |
| Helical region | 490 | |
| Beta-strand region | 487 | |
| Hydrogen bonded turn | 484 | |
| Helical region | 464 | ************* |
| 000111 1 | 463 | ****************** |
| PROTEIN-TYROSINE PHOSPHATASE | . 463 | *************************************** |
| Query: | 647 | / QTLIARKRAEEQSLQVGREYTNIKYTGEIGNDSQRSPLPP 686 |
| | 500 | +TL R E++S + G EYTNIKY+ +SPLPP B ETLQRRIEEEQKSKRKGHEYTNIKYSLADQTSGDQSPLPP 562 |
| Sbjct: | 548 | |
| Conflict | 542 | |
| phosphorylation | 533 | |
| Conflict | 52 | |
| Hydrogen bonded turn | | 3 * |
| Helical region | | 3 +++++++++++++++++++++++++++++++++++++ |
| PTPN11 | J2. | w |

FIGURE 3







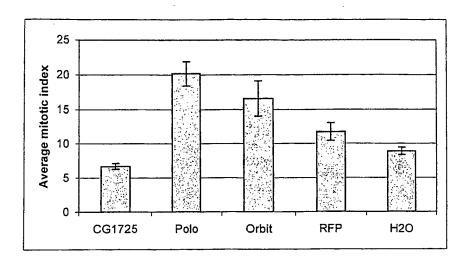


FIGURE 6A

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 1

BLAST P sequence alignment

Score = 616 bits (1588), Expect = e-175 Identities = 306/517 (59%), Positives = 390/517 (75%), Gaps = 24/517 (4%)

```
Ulaccession
            THE REPORT OF THE PROPERTY.
Query: 453 QPGSRYASTNVLAAVPPGTPRAVST-----EDITREPRTITIQKGPQGLGFNIVGGE 504
                                            ++ITREPR + + +G GLGFNIVGGE
               + S +
                          P +P S
           QP
Sbjct: 425 QPVDNHVSPSSFLGQTPASPARYSPVSKAVLGDDEITREPRKVVLHRGSTGLGFNIVGGE 484
Query: 505 DGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTLLAQ 564
           DG+GI++SFILAGGPADL EL++GD+++SVN+V+L A+HE+AA ALK +G VT++AQ
Sbjct: 485 DGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAALKNAGQAVTIVAQ 544
Query: 565 YRPEEYNRFEARIQELKQQXXXXXXXXXXXXXXXXXVTXQKRSLYVRALFDYDPNRDDGLPSRG 623
                                              QKRSLYVRALFDYD +D GLPS+G
           YRPEEY+RFEA+I +L++Q
Sbjct: 545 YRPEEYSRFEAKIHDLREQMMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLPSQG 604
Query: 624 LPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSVKFQGHA 683
           L FK GDILHV NASDDEWWQAR+V D E +++G++PSKRR E+K RAR ++VKF
Sbjct: 605 LNFKFGDILHVINASDDEWWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTVKFN--- 661
Query: 684 AANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEIDIXXXXX 743
+ DK + + K+K FSRKFPF K++D+ ++ SD + + V S+ S+ +
Sbjct: 662 -- SKTRDKGQSFNDKRKKNLFSRKFPFYKNKDQSEQETSDADQH-VTSNASDSE----- 712
Query: 744 XXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYPDKFGSCVPHTT 803
                       VLSYE V + +NYTRPVIILGP+KDRINDDLISE+PDKFGSCVPHTT
Sbjct: 713 ---SSYRGQEEYVLSYEPVNQQEVNYTRPVIILGPMKDRINDDLISEFPDKFGSCVPHTT 769
Query: 804 RPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVAEKGKHCI 863
           RPKR+YEVDGRDYHFV+SREQME+DIQ H FIEAGQYN++LYGTSV SVREVA KGKHCI
Sbjct: 770 RPKRDYEVDGRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAGKGKHCI 829
Query: 864 LDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAKKTYERAIKMEQEFGEY 923
           LDVSGNAIKRLQ+AQLYP+++FIKPKS++++MEMN+R+TEEQA+KT+ERA+K+EQEF E+
Sbjct: 830 LDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLTEEQARKTFERAMKLEQEFTEH 889
Query: 924 FTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
           FT +VQGDT+E+IY++VK +I QSG IWVP+KE L
Sbjct: 890 FTAIVQGDTLEDIYNQVKQIIEEQSGSYIWVPAKEKL 926
Score = 206 bits (524), Expect = 2e-51
Identities = 119/227 (52%), Positives = 146/227 (63%), Gaps = 30/227 (13%)
```



Query: 197 DGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIGK 243
DG+L IGDKL+AV + LE VTHE AV LK+ +D V L + K
Sbjct: 362 DGKLQIGDKLLAV----NNVCLEEVTHEEAVTALKNTSDFVYLKVAK 404
Score = 88.2 bits (217), Expect = 7e-16
Identities = 68/234 (29%), Positives = 95/234 (40%), Gaps = 43/234 (18%)

Query: 40 DIQLERGNSGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXXXXXX 99 +I+L +G GLGFSIAGG N HI D SIY+TK+I GGAA DG+L Sbjct: 319 EIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVC 378 Query: 100 XXXXPHASAVDALKKAGNVVKLHVKRKXXXXXXXXXXXXXXXXXXXXXXXXXXVVI----- 153 H AV ALK + V L V + V Sbjct: 379 LEEVTHEEAVTALKNTSDFVYLKVAKPTSMYMNDGYAPPDITNSSSQPVDNHVSPSSFLG 438 Query: 154 -----------------EIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVT 186 ++ L +G GLGF+I GG + GI+++ Sbjct: 439 QTPASPARYSPVSKAVLGDDEITREPRKVVLHRGSTGLGFNIVGGEDGE------GIFIS 492 Query: 187 KLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLI 240 + GG A + G L GD++I+V + L +HE A A LK+ VT++ Sbjct: 493 FILAGGPADLSGELRKGDRIISV----NSVDLRAASHEQAAAALKNAGQAVTIV 542 Score = 70.1 bits (170), Expect = 2e-10 Identities = 47/141 (33%), Positives = 69/141 (48%), Gaps = 12/141 (8%)

Query: 432 MPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITREPRTITIQK 491 +T+ L TP V+ D E IT+++ +P LPV + T PO P Sbjct: 176 IPVLPVPAENTVILPTIPQANPPPV-LVNTDSLE----TPTYVNGTDADYEYEEITLER 229 Query: 492 GPQGLGFNIVGGEDG-----QGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATH 545 G GLGF+I GG D I+++ I+ GG A L+ D +L VN V++ TH Sbjct: 230 GNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILQVNEVDVRDVTH 289 Query: 546 EEAAQALKTSGGVVTLLAQYR 566 +A +ALK +G +V L + R Sbjct: 290 SKAVEALKEAGSIVRLYVKRR 310 Score = 67.4 bits (163), Expect = 1e-09Identities = 39/81 (48%), Positives = 49/81 (60%), Gaps = 6/81 (7%)

<u>Lesons</u>

Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540 I + KGP+GLGF+I GG Q IYV+ I+ GG A +L+ GD+LL+VNNV L Sbjct: 320 IKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCL 379

Query: 541 THATHEEAAQALKTSGGVVTL 561 THEEA ALK + V L Sbjct: 380 EEVTHEEAVTALKNTSDFVYL 400

FIGURE 6B

CLUSTAL W (1.82) sequence alignment

| Drosophila Human | MTTRKKKRDGGGSGGGFIKKVSSLFNLDSVNGDDSWLYEDIQLERGNSGLGFSIAGGTDN MPVRKQDTQRALHLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ ***: | 60 47 |
|---------------------|--|------------|
| Drosophila Human | PHIGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVK ALIDIQEFYEVTLLDNPKCID-RSKPSEPIQPVNTWEISSLPSSTVTSETLPSSLSPS . *.: :* * * * : * : * : | |
| Drosophila Kuman | LHVKRKRGTATTPAAGSAAGDARDSAASGPKVIEIDLVKGGKGLGFSIAGGIGNQHIPGD VEKYRYQDEDTPPQEHISPQITNEVIGPELVHVSEKNLSEIENVHGFVSHSHIS-P :. * :. * .* : **:::: : | 180 159 |
| Drosophila Human | NGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKV IKPTEAVLPSPPTVPVIPVLPVPAENTVILPTIPQANPPPVLVNTDSLETPTYVNGTDAD : * * *.: : .: .: * : * * . ** | 237 219 |
| Drosophila Human | TLIIGKTQHLTTSASGGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHATPMVNS YEYEEITLERGNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILQV * * ** *:: * ::: * :: :::::::: | 293 279 |
| Drosophila Human | QSTGALNSMGQTVVDSPSIPQAAAAVAAAANASASASVIASNNTISNTTVTTVTATATAS NEVDVRDVTHSKAVEALKEAGSIVRLYVKRRKPVSEKIMEIK-LIKGPKGLGFSIAGGVG ::*:: :* :: :* :: :* | 353 338 |
| Drosophila Human | NDSSKLPPSLGANSSISISNSNSNSNSNNINNINSINNNNSSSSSTTATVAAATPTAASA NQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCLEEVTHEEAVTALKNTSDFV *: *: *. :::::::::::::::::::::::::: | 413 398 |
| Drosophila Human | AAAAASSPPANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPR YLKVAK-PTSMYMNDGYAPPDITNSSSQPVDNHVSPSS-FLGQTPASPARYSPVSKA .*. *.: :: .: .* ** .* . * * * * | 473 453 |
| Drosophila Human | AVSTEDITREPRTITIQKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLL VLGDDEITREPRKVVLHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRII .:::******.:::*.********************* | 533 513 |
| Drosophila Human | SVNNVNLTHATHEEAAQALKTSGGVVTLLAQYRPEEYNRFEARIQELKQQAALGAGGSGT SVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLREQMMNSSISSGS ***.*: *:**:** ***: ***:*************** | 593 573 |
| Drosophila Human | -LLRTTQKRSLYVRALFDYDPNRDDGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDN GSLRTSQKRSLYVRALFDYDKTKDSGLPSQGLNFKFGDILHVINASDDEWWQARQVTPDG ***:********************************* | 652 633 |
| Drosophila Human | EDEQIGIVPSKRRWERKMRARDRSVKFQGHAAANNNLDKQSTLDRKKKNFTFSRKFPFMK ESDEVGVIPSKRRVEKKERARLKTVKFNSKTRDKGQSFNDKRKKNLFSRKFPFYK *.:::*::**** *:* *** ::***: .:. ** .::: *:*: ****** * | |
| Drosophila Human | SRDEKNEDGSDQEPNGVVSSTSEIDINNVNNNQSNEPQPSEENVLSYEAVQRLSINYTRP NKDQSEQETSDADQH-VTSNASDSESSYRGQEEYVLSYEPVNQQEVNYTRP .:*:::: ** :: *.*:*: :: ** ******** | 772 738 |
| Drosophila Human | VIILGPLKDRINDDLISEYPDKFGSCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNH VIILGPMKDRINDDLISEFPDKFGSCVPHTTRPKRDYEVDGRDYHFVTSREQMEKDIQEH *****:******************************* | 798 |
| Drosophila Human | LFIEAGQYNDNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVD KFIEAGQYNNHLYGTSVQSVREVAGKGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSME ******::***** ****** ***************** | 892 858 |
| Drosophila Human | SVMEMNRRMTEEQAKKTYERAIKMEQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTI NIMEMNKRLTEEQARKTFERAMKLEQEFTEHFTAIVQGDTLEDIYNQVKQIIEEQSGSYI .:****:*:****:**.:**.:**.:**.:**.:**.:* | 918 |

Drosophila Human

WVPSKESL 960 WVPAKEKL 926 ***:**.*

FIGURE 6C

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 2

BLASTP sequence alignment

Score = 621 bits (1601), Expect = e-176
Identities = 318/524 (60%), Positives = 390/524 (73%), Gaps = 43/524 (8%)

```
Query: 438 ESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITREPRTITIQKGPQGLG 497
           +S. T++
                   S ROP
                                             RAVS E
                                                       EPR + + KG GLG
Sbjct: 389 DSEMTSHSQHSTATRQPSMTLQ------RAVSLEG---EPRKVVLHKGSTGLG 432
Query: 498 FNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGG 557
           FNIVGGEDG+GI+VSFILAGGPADL EL+RGDQ+LSVN ++L A+HE+AA ALK +G
Sbjct: 433 FNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQ 492
Query: 558 VVTLLAQYRPEEYNRFEARIQELKQQXXXXXXXXXXXXXXXXXOKRSLYVRALFDYDPNRD 616
           VT++AQY+PE+Y RFEA+I +L++Q
                                                    OKRSLYVRA+FDYD ++D
Sbjct: 493 TVTIIAQYQPEDYARFEAKIHDLREQMMNHSMSSGSGSLRTNQKRSLYVRAMFDYDKSKD 552
Query: 617 DGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRS 676
           GLPS+GL FK+GDILHV NASDDEWWQARRV+ + + E++G++PSKRR ERK RAR ++
Sbjct: 553 SGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKT 612
Query: 677 VKFQGHAAANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEI 736
          VKF
                    ++ K S D++KK+F FSRKFPF K++++ ++ SD E
Sbjct: 613 VKFNAKPGVIDS--KGSFNDKRKKSFIFSRKFPFYKNKEQSEQETSDPE-
Query: 737 DIXXXXXXXXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYPDKFG 796
                             +LSYE V R INYTRPVIILGP+KDRINDDLISE+PDKFG
Sbjct: 664 DL------ILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFG 706
Query: 797 SCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVA 856
          SCVPHTTRPKR+YEVDGRDYHFV SREOME+DIQ H FIEAGOYNDNLYGTSV SVR VA
Sbjct: 707 SCVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRFVA 766
Query: 857 EKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAKKTYERAIKM 916
          E+GKHCILDVSGNAIKRLQVAQLYP+A+FIKP+S++S+MEMN+R+TEEQAKKTY+RAIK+
Sbjct: 767 ERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLMEMNKRLTEEQAKKTYDRAIKL 826
Query: 917 EQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960
          EQEFGEYFT +VQGDT+E+IY++ K +I QSGP IW+PSKE L
Sbjct: 827 EQEFGEYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870
Score = 197 bits (502), Expect = 7e-49
Identities = 111/221 (50%), Positives = 140/221 (63%), Gaps = 24/221 (10%)
```



12/19 V+EI L KG KGLGFSIAGG+GNQHIPGDN IYVTK+ DGG AQ DGRL Sbjct: 191 ------VVEIKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQ 240 Query: 202 IGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242 + +LE VTHE AVA LK+ ++ V L +G +GD+L+ V Sbjct: 241 VGDRLLMV----NNYSLEEVTHEEAVAILKNTSEVVYLKVG 277 Score = 66.2 bits (160), Expect = 3e-09 Identities = 40/125 (32%), Positives = 64/125 (51%), Gaps = 11/125 (8%) Query: 448 SPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITREPRTITIQKGPQGLGFNIVGGEDGQ 507 +T+ L +P V+ +I E IT+++G GLGF+I GG D P SP Sbjct: 65 SPLKASPAPIIVNTDTLDTIP----YVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNP 119 Query: 508 -----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561 L+ D +L VN V+++ +H +A +ALK +G + L GI+++ I+ GG A Sbjct: 120 HIGDDPGIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARL 179 Query: 562 LAQYR 566 + R Sbjct: 180 YVRRR 184 Score = 65.5 bits (158), Expect = 5e-09Identities = 38/81 (46%), Positives = 47/81 (57%), Gaps = 6/81 (7%) ---GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540 Query: 487 ITIQKGPQGLGFNIVGGEDGQ-I + KGP+GLGF+I GG Q IYV+ I+ GG A L+ GD+LL VNN +L Sbjct: 194 IKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQVGDRLLMVNNYSL 253 Query: 541 THATHEEAAQALKTSGGVVTL 561 THEEA LK + VV L Sbjct: 254 EEVTHEEAVAILKNTSEVVYL 274 Score = 50.8 bits (120), Expect = 1e-04Identities = 33/87 (37%), Positives = 48/87 (54%), Gaps = 10/87 (11%) 1535 Query: 154 EIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNG 213 ++ L KG GLGF+I GG + GI+V+ + GG A + G L GD++++V NG Sbjct: 421 KVVLHKGSTGLGFNIVGGEDGE-----GIFVSFILAGGPADLSGELQRGDQILSV--NG 472 Query: 214 SEKNLENVTHELAVATLKSITDKVTLI 240 + L +HE A A LK VT+I Sbict: 473 ID--LRGASHEQAAAALKGAGQTVTII 497 Score = 41.2 bits (95), Expect = 0.10Identities = 24/81 (29%), Positives = 36/81 (43%), Gaps = 6/81 (7%) र्वा <u>। इंड विशेष</u> क्षेत्र होने हे शहर है

Query: 41 IQLERGNSGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 100 + L +G++GLGF+I GG D I+++ +++GG A G L

Sbjct: 422 VVLHKGSTGLGFNIVGGEDG-----EGIFVSFILAGGPADLSGELQRGDQILSVNGIDL 475

Query: 101 XXXPHASAVDALKKAGNVVKL 121 H A ALK AG V + Sbjct: 476 RGASHEQAAAALKGAGQTVTI 496

FIGURE 6D

CLUSTAL W (1.82) sequence alignment

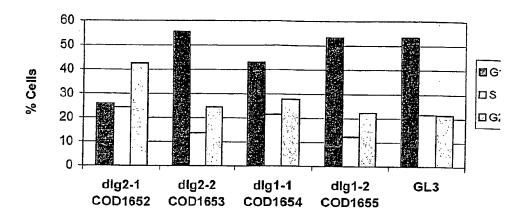
| Drosophila Human | MTTRKKKRDGG | |
|---------------------|--|------------|
| Drosophila Human | GSGGGFIKKVSSLFNLDSVNG-DDSWLYEDIQLERGNSGLGFSIAGGTDNPH QSHISPLKASPAPIIVNTDTLDTIPYVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNPH .* . :* : . : * : : : : : * : * * * * * | |
| Drosophila Human | IGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVKLH IGDDPGIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLY ** **:**:*.***** **** :** *: **:*.* :**:**:**:**:**: | |
| Drosophila Human | VKRKRGTATTPAAGSAAGDARDSAASGPKVIEIDLVKGGKGLGFSIAGGIGNQHIPGDNG VRRRRPILETVVEIKLFKGPKGLGFSIAGGVGNQHIPGDNS *:*: * *:*:*************************** | |
| Drosophila Human | IYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG IYVTKIIDGGAAQKDGRLQVGDRLLMVNNYSLEEVTHEEAVAILKNTSEVVYLKVG ****: *** ** ****::**: ***:**** *** | 242 277 |
| Drosophila Human | KTQHLTTSASGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHATPMVNSQSTGALNSM NPTTIYMTDPYGPPDITHSYSPPMEN :.::* :::** :::.** | 302 303 |
| Drosophila Human | GQTVVDSPSIPQAAAAVAAAANASASASVIASNNTISNTTVTTVTATATASNDSSKLPPSGTLEYKTSLPPIS :::.** .*.:* * | 362 323 |
| Drosophila Human | LGANSSISISNSNSNSNNNNNNNNSINNNNSSSSSTTATVAAATPTAASAAAAAASSPP PGRYSPIPKHMLVDDDYTRPPEPVYSTVNKLCDKPASPRHYSPVECDKSFLL * *.*. :: : : * *: *:* * * | 422 375 |
| Drosophila Human | ANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAVPPGTPRAVSTEDITR S-APYSHYHLGLLP-DSEMTSHSQHSTATRQPSMTLQRAVSLEG : : *: : ** : *: .: .: ** .** | 482 417 |
| Drosophila Human | EPRTITIQKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTH EPRKVVLHKGSTGLGFNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRG ***.:::**. **************************** | 542 477 |
| Drosophila Human | ATHEEAAQALKTSGGVVTLLAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKR ASHEQAAAALKGAGQTVTIIAQYQPEDYARFEAKIHDLREQMMNHSMSSGSGSLRTNQKR *:**:** *** : * .**::***:** ***:*::* : . **: ***.*** | 601 537 |
| Drosophila Human | SLYVRALFDYDPNRDDGLPSRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVP SLYVRAMFDYDKSKDSGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIP *****:**** :: .: .: *: .**: ****** ******** | |
| Drosophila Human | SKRRWERKMRARDRSVKFQGHAAANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDG SKRRVERKERARLKTVKFNAKPGVIDSKGSFNDKRKKSFIFSRKFPFYKNKEQSEQET *** *** *** ::**:::::::::::::::::::::: | |
| Drosophila Human | SDQEPNGVVSSTSEIDINNVNNNQSNEPQPSEENVLSYEAVQRLSINYTRPVIILGPLKD SDPERGQEDLILSYEPVTRQEINYTRPVIILGPMKD ** * : .*::****.* .*********:** | 781 691 |
| Drosophila Human | RINDDLISEYPDKFGSCVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYN RINDDLISEFPDKFGSCVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYN *******:***************************** | 841 751 |
| Drosophila Human | DNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRM DNLYGTSVQSVRFVAERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLMEMNKRL | 901 811 |
| Drosophila Human | TEEQAKKTYERAIKMEQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL TEEQAKKTYDRAIKLEQEFGEYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL ********:***:************************ | 960 870 |

| Hu-Dlg1 | MPVRKQDTQRALHLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ-ALIDIQEFY | 56 |
|---------|--|-----|
| Hu-Dlg4 | MSQRPRAPRSALWLLAPPLLRWAPPLLTVLHSDLFQ-ALLDILDYY | |
| Hu-Dlg2 | MFFACYCALRTNVKKYRYQDEDAPHDHSLPRLTHEVRGP-ELVHVSEK- | |
| Hu-Dlq3 | | |
| - | MHKHQHCCKCPECYEVTRLAALRRLEPPGYGDWQVPDPYGPGGGNGASAGYGGYS | |
| Dm-Dlg1 | MTTRKKKRDGGKRDGG | 11 |
| Hu-Dlg5 | | |
| | | |
| Hu-Dlgl | EVTLLDNPKCIDRSKPSEPIQPVNTWEISSLPSSTVTSETLPSSLSPSVEKYRYQDEDTP | 116 |
| Hu-Dlg4 | | 63 |
| Hu-Dlg2 | NLSQIENVHGYVLQSHISP | - |
| Hu-Dlg3 | SQTLPSQAGATPTPRTKAKLIP | |
| - | | ,, |
| Dm-Dlg1 | | |
| Hu-Dlg5 | * | |
| | | |
| Hu-Dlgl | PQEHISPQITNEVIGPELVHVSEKNLSEIENVHGFVSHSHISPIKPTEAVLPSPPTVPVI | |
| Hu-Dlg4 | PLEHSPAHLPN | 74 |
| Hu-Dlg2 | LK | 68 |
| Hu-Dlg3 | TGRDVGPVPLKPVPGK | 93 |
| Dm-Dlg1 | | |
| Hu-Dlg5 | *************************************** | |
| . Digo | | |
| Hu-Dlg1 | PVLPVPAENTVILPTIPQANPPPVLVNTDSLETPTYVNGTDADYEYEEITLERGNSG | 223 |
| - | | |
| Hu-Dlg4 | QANSPPVIVNTDTLEAPGYELQVNGTEGEMEYEEITLERGNSG | |
| lu-Dlg2 | YVNGTEIEYEFEEITLERGNSG | |
| łu-Dlg3 | STPKLNGSGPSWWPECTCTNRDWYEQVNGSDGMFKYEEIVLERGNSG | |
| Dm-Dlgl | SVNGDD-SWLYEDIQLERGNSG | 49 |
| iu-Dlg5 | mrathgsnslpssarlgsssn | 21 |
| | · · · · · · · · · · · · · · · · · · · | |
| Iu-Dlg1 | LGFSIAGGTDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILQVNEVDVRDVTHSKAV | 293 |
| łu-Dlg4 | LGFSIAGGTDNPHIGDDPSIFITKIIPGGAAAQDGRLRVNDSILFVNEVDVREVTHSAAV | |
| iu-Dlg2 | LGFSIAGGTDNPHIGDDPGIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAV | |
| - | | |
| iu-Dlg3 | LGFSIAGGIDNPHVPDDPGIFITKIIPGGAAAMDGRLGVNDCVLRVNEVEVSEVVHSRAV | |
| Dm-Dlg1 | LGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAV | |
| lu-Dlg5 | LQFKAER-IKIPSTPRYPRSVVGSERGSVSHSECSTPPQSPLNIDTLSSCSQSQTSAS | 78 |
| | * * * | |
| lu-Dlg1 | EALKEAGSIVRLYVKRRKPVSEKIMEIKLIKGPKGLGFSI | 333 |
| lu-Dlg4 | EALKEAGSIVRLYVMRRKPPAEKVMEIKLIKGPKGLGFSI | |
| lu-Dlg2 | EALKEAGSIARLYVRRRRPILETVVEIKLFKGPKGLGFSI | |
| lu-Dlq3 | EALKEAGPVVRLVVRRRQPPPETIMEVNLLKGPKGLGFSI | 240 |
| - | | |
| m-Dlgl | DALKKAGNVVKLHVKRKR-GTATTPAAGSAAGDARDSAASGPKVIEIDLVKGGKGLGFSI | |
| lu-Dlg5 | TLPRIAVNPASLGERRKDRPYVEEPRHVKVQKGSEPLGISI | 119 |
| | : * . * *:!.: ** : **:** | |
| Ku-Dlg1 | AGGVGNQHIPGDNSIYVTKIIEGGAAHKDGKLQIGDKLLAVNNVCLEEVTHEEAVT | 389 |
| Iu-Dlg4 | AGGVGNQHIPGDNSIYVTKIIEGGAAHKDGRLQIGDKILAVNSVGLEDVMHEDAVA | |
| Iu-Dlg2 | AGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQVGDRLLMVNNYSLEEVTHEEAVA | |
| | | |
| Iu-Dlg3 | AGGIGNQHIPGDNSIYITKIIEGGAAQKDGRLQIGDRLLAVNNTNLQDVRHEEAVA | |
| m-Dlg1 | AGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVA | |
| Iu-Dlg5 | VSGEKGGIYVSKVTVGSIAHQAG-LEYGDQLLEFNGINLRSATEQQARL***::*: * . *: * * . **::: *: * | 167 |
| | | |
| łu-Dlgl | ALKNTSDFVYLKVAKPTSMYMNDGYA | |
| iu-Dlg4 | ALKNTYDVVYLKVAKPSNAYLSDSYA | |
| Iu-Dlg2 | ILKNTSEVVYLKVGNPTTIYMTDPYG | |
| iu-Dlg3 | SLKNTSDMVYLKVAKPGSLHLNDMYA | 322 |
| Dm-Dlg1 | TLKSITDKVTLIIGKTQHLTTSASGGGGGGLSSGQQLSQSQSQLATSQSQSQVHQQQHAT | |
| Nu-Dlg5 | IIGOOCDTITILAQYNPHVHQLSSHS | |
| m .nrda | : . : : : | 133 |
| | | |
| Iu-Dlgl | | |
| Iu-Dlg4 | | |
| lu-Dlg2 | | |
| Iu-Dlg3 | | |
| Dm-Dlal | PMVNSOSTGAI.NSMGOTVVDSPSIPOAAAAVAAAANASASASVIASNNTISNTTVTTVTA | 348 |

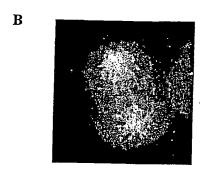
15/19

| Hu-Dlg5 | | |
|--------------|---|------|
| | | |
| Hu-Dlq1 | PSSFLG | 420 |
| Hu-Dlg4 | DI DI MOCACA DATA | 430 |
| | PPDITTSYSQHLDNEISHSSYLGTDYP | 326 |
| Hu-Dlg2 | SGNNGTLEYK | 316 |
| Hu-Dlg3 | PPDYASTFTALADNHISHNSSLGYLGAVESKVSY | 356 |
| Dm-Dlg1 | TATASNDSSKLPPSLGANSSISISNSNSNSNSNNINNINSINNNNSSSSSTTATVAAATP | 408 |
| Hu-Dlq5 | GSGTTTPEHPSVIDPLM | |
| | | 220 |
| | * | |
| Hu-Dlg1 | QTPASPARYSPVSKAVLGDDEITR | 460 |
| Hu-Dlg4 | MAMPHO DO DO PORA LA CONTROLLA DE LA CONTROLLA | 462 |
| | TAMTPTSPRRYSPVAKDLLGEEDIPR | 352 |
| Hu-Dlg2 | TSLPPISPGRYSPIPKHMLVDDDYTRPPEPVYSTVNKLCDKPASPRHYSPVECDKSFLLS | 376 |
| Hu-Dlg3 | PAPPQVPPTRYSPIPRHMLAEEDFTR | 382 |
| Dm-Dlgl | TAASAAAAASSPPANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTN | 462 |
| Hu-Dlg5 | EQDEGPSTPPAKQSSSRIAGDANKKT | 252 |
| , | | 232 |
| | | |
| Hu-Dlg1 | EPRKVVLHRGSTGLGFNIV | 481 |
| Hu-Dlg4 | EPRRIVIHRGSTGLGFNIV | 371 |
| Hu-Dlg2 | APYSHYHLGLLPDSEMTSHSQHSTATRQPSMTLQRAVSLEGEPRKVVLHKGSTGLGFNIV | 426 |
| Hu-Dlg3 | EPRKIILHKGSTGLGFNIV | 430 |
| Dm-Dlg1 | EPRRIILHRGSTGLGFNIV | 401 |
| | VLAAVPPGTPRAVSTEDITREPRTITIQKGPQGLGFNIV | 501 |
| Hu-Dlg5 | LEPRVVFIKKSQLELGVHLC | 272 |
| | *** : :::. **.:: | |
| Hu-Dlg1 | CCEDCECTET CETT ACCDADT CCET DVCDDY TOUNGUET DAY COMPANDA DAY | |
| | GGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAALKNAGQAVTI | 541 |
| Hu-Dlg4 | GGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAIALKNAGQTVTI | 431 |
| Hu-Dlg2 | GGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQTVTI | 496 |
| Hu-Dlg3 | GGEDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLRNATHEQAAAALKRAGQSVTI | 461 |
| Dm-Dlg1 | GGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL | 561 |
| Hu-Dlg5 | GG-NLHGVFVAEVEDDSPAKGPDGLVPGDLILEYGSLDVRNKTVEEVYVEMLKPRDGVRL | 331 |
| | ** : .*:::: :** * ** ::::: : *:. : . * : | JJ1 |
| | | |
| Hu-Dlgl | VAQYRPEEYSRFEAKIHDLREQMMNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLP | 601 |
| Hu-Dlg4 | IAQYKPEEYSRFEAKIHDLREQLMNSSLGSGTASLRSNPKRGFYIRALFDYDKTKDCGFL | 491 |
| Hu-Dlg2 | IAQYQPEDYARFEAKIHDLREQMMNHSMSSGSGSLRTNQKRSLYVRAMFDYDKSKDSGLP | 556 |
| Hu-Dlg3 | VAQYRPEEYSRFESKIHDLREQMMNSSMSSGSGLRTSEKRSLYVRALFDYDRTRDSCLP | 533 |
| Dm-Dlgl | LAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKRSLYVRALFDYDPNRDDGLP | 521 |
| | MUNICIPALITY NO. | 620 |
| Hu-Dlg5 | KVQYRPEEFTKAKGLADV | 363 |
| | ·**:**:: ::*:**::* | |
| Hu-Dlg1 | SQGLNFKFGDILHVINASDDEWWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTV | c= 0 |
| Hu-Dlg4 | SOLICE SCOUL WITH SDE - EMPORAÇVI FDGESDEVQI PSKRKVERREKARLKIV | 658 |
| - | SQALSFRFGDVLHVIDASDEEWWQARRVHSDSETDDIGFIPSKRRVERREWSRLKAK | 548 |
| Hu-Dlg2 | SQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKTV | 613 |
| Hu-Dlg3 | SQGLSFSYGDILHVINASDDEWWQARLVTPHGESEQIGVIPSKKRVEKKERARLKTV | 578 |
| Dm-Dlgl | SRGLPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSV | 677 |
| Hu-Dlg5 | EQELSFKKDDILYVDDTLPQGTFGSWMAWQLDENAQKIQRGQIPSKYVMDQEFSRRLSMS | 423 |
| - | .: * * .*:*:* : : * * : . : : * : : * | |
| | | |
| Hu-Dlgl | KFNSKTRDKGQSFNDKRKKNLFSRKFPFYKNKDQSEQETSDADQH | 703 |
| Hu-Dlg4 | DWG | 551 |
| Hu-Dlg2 | KFNAKPGVIDSKGSFNDKRKKSFIFSRKFPFYKNKEQSEQE | |
| Hu-Dlg3 | KFHARTGMIESNRDFPGLSDDYY | 601 |
| Dm-Dlg1 | KFQGHAAANNNLDKQSTLDRKKKNFTFSRKFPFMKSRDEKNEDGSDQEPNGVVSSTSEID | POT |
| Hu-Dlg5 | PUNDONG MEMICA A A PROGREDANIA MANGEL EFFINANCE AND CONTROL OF STREET | 131 |
| nu-Digo | EVKDDNSATKTLSAAARRSFFRRKHKHKRSGSKDGKDLLALDAFS | 468 |
| | | |
| Hu-Dlg1 | VTSNASDSESSYRGQEEYVLSYEPVNQQEVNYTRPVIILGPMKDRINDDLISEFPDKFGS | 763 |
| Hu-Dlg4 | SSSGSQGREDSVLSYETVTQMEVHYARPIIILGPTKDRANDDLLSEFPDKFGS | 604 |
| Hu-Dlg2 | TTSDPERCOEDLII SVEDVTDORTNUMBRUTTI CRIMIDATIVANI TORMONI | 204 |
| | TSDPERGQEDLILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFGS | 107 |
| Hu-Dlg3 | GAKNLKGQEDAILSYEPVTRQEIHYARPVIILGPMKDRVNDDLISEFPHKFGS | 654 |
| Dm-Dlg1 | INNVNNNQSNEPQPSEENVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYPDKFGS | 797 |
| Hu-Dlg5 | SDSIPLFEDSVSLAYQRVQKVDCTALRPVLILGPLLDVVKEMLVNEAPGKFCR | 521 |
| , | . :. *:*: * : . **::*** * :: *:.* * ** | |
| Huani al | CUDUMED DED DACTOUCH DATE OF THE PROPERTY OF TH | |
| Hu-Dlg1 | CVPHTTRPKRDYEVDGRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAG | 823 |
| Hu-Dlg4 | CVPHTTRPKREYEIDGRDYHFVSSREKMEKDIQAHKFIEAGQYNSHLYGTSVQSVREVAE | 664 |
| Hu-Dlg2 | CVPHTTRPKRDYEVDGRDYHFVISREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRFVAE | 767 |
| Hu-Dlg3 | CVPHTTRPRRDNEVDGQDYHFVVSREQMEKDIQDNKFIEAGQFNDNLYGTSIQSVRAVAE | 714 |
| Dm-Dlg1 | CVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVAE | 857 |
| Hu-Dlg5 | CPLEVMKASQQAIERGVKDCLFVDYKRRSGHFDVTTVASIXEITE | 566 |
| - | | |

| | * : *:: *:: *:: *:: *:: *:: *:: *:: * |
|--|--|
| Hu-Dlg1 Hu-Dlg4 Hu-Dlg2 Hu-Dlg3 Dm-Dlg1 Hu-Dlg5 | KGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLTEEQARKTFE 877 QGKHCILDVSANAVRRLQAAHLHPIAIFIRPRSLENVLEINKRITEEQARKAFD 718 RGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLESLMEMNKRQTTEQAKKTYD 821 RGKHCILDVSGNAIKRLQQAQLYPIAIFIKPKSIEALMEMNRRQTYEQANKIYD 768 KGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAKKTYE 911 KNRHCLLDIAPHAIERLHHMHIYPIVIFIHYKSAKHIKEQRDPIYLRDKVTQRHSKEQFE 626 :.:**:**:::::::::::::::::::::::::::::: |
| Hu-Dlg1 Hu-Dlg4 Hu-Dlg2 Hu-Dlg3 Dm-Dlg1 Hu-Dlg5 | RAMKLEQEFTEHFTAIVQGDTLEDIYNQVKQIIEEQSGSYIWVPAKEKL 926 RATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERL 767 RAIKLEQEFGEYFTAIVQGDTLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870 KAMKLEQEFGEYFTAIVQGDSLEEIYNKIKQIIEDQSGHYIWVPSPEKL 817 RAIKMEQEFGEYFTGVVQGDTIEEIYSKVKSMIWSQSGPTIWVPSKESL 960 AAQKLEQEYSRYFTGVIQGGALSSICTQILAMVNQEQNKVLWIPACPL- 674 * *:***: |



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